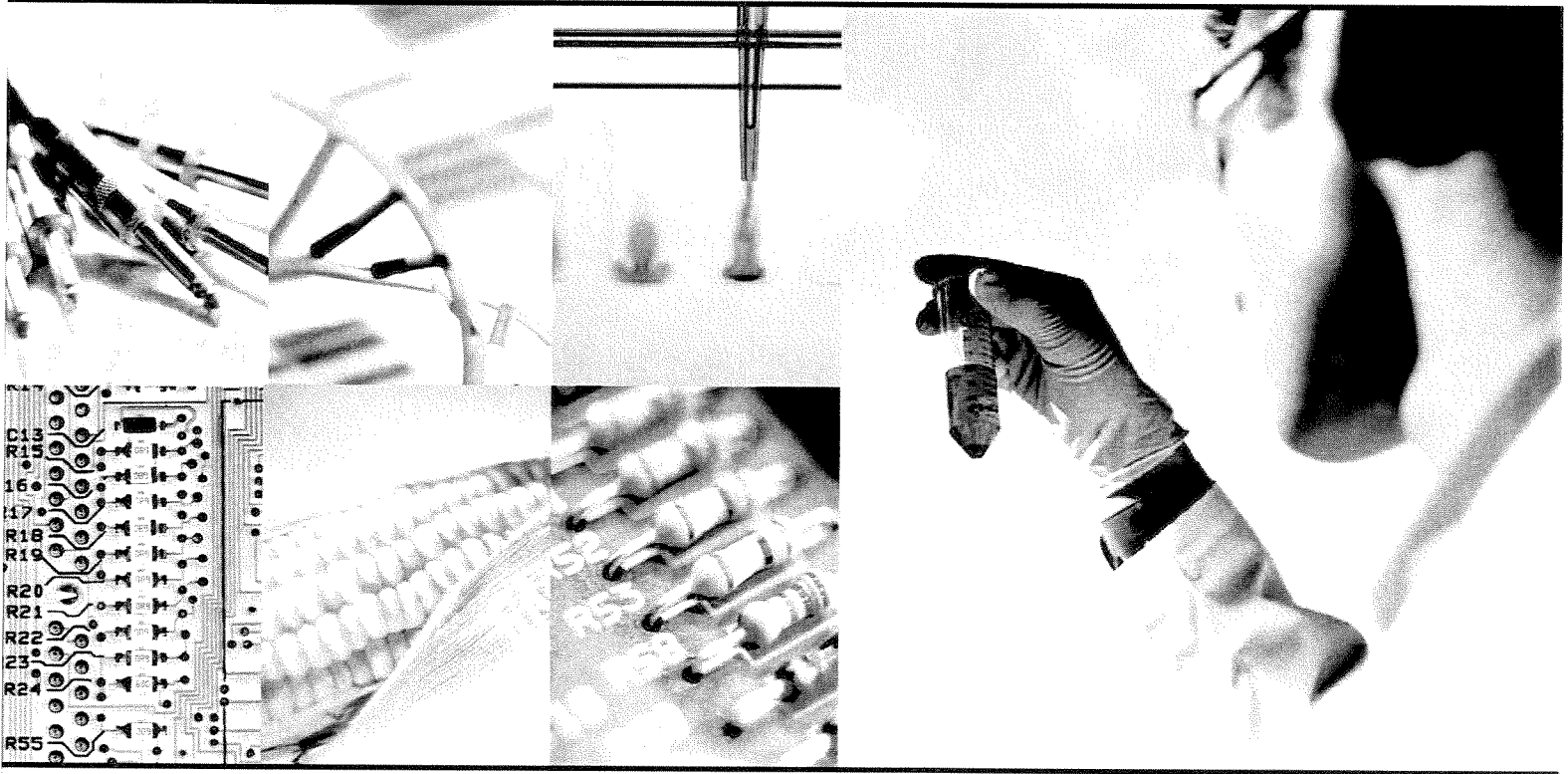


WRITTEN DESCRIPTION TRAINING MATERIALS



EXAMPLE 4: EXPRESSED SEQUENCE TAGS (ESTs)

4A: EFFECT OF OPEN TRANSITIONAL LANGUAGE

Specification:

The specification discloses SEQ ID NO: 16, which is an EST, *i.e.*, a cDNA that corresponds to only part of a protein-encoding open reading frame (ORF). The specification does not address whether the cDNA crosses an exon/intron splice junction. The specification provides a working example in which the cDNA of SEQ ID NO: 16 was isolated from a yeast cDNA library and sequenced. The specification discloses that SEQ ID NO: 16 will hybridize to its complement in yeast genomic DNA and that the cDNA is useful for identifying yeast infections.

Claim:

Claim 1. An isolated DNA comprising SEQ ID NO: 16.

Analysis:

Claim 1

Claim 1 is directed to the genus of DNAs comprising the cDNA sequence described in the specification as SEQ ID NO: 16; the claimed DNAs may also include additional DNA sequences attached to either end of the sequence shown in SEQ ID NO: 16. The claimed genus therefore includes the full-length open reading frame (ORF) that includes SEQ ID NO: 16, as well as fusion constructs and vectors comprising SEQ ID NO: 16. (The genus might include the full-length genomic gene. More specifically, if SEQ ID NO: 16 is derived from a single exon, the genomic sequence would comprise SEQ ID NO: 16; if SEQ ID NO: 16 is derived from more than one exon, the genomic sequence would not comprise SEQ ID NO: 16.)

There may be substantial variability among the species of DNAs encompassed by the scope of the claim because SEQ ID NO: 16 may be combined with other DNA sequences, how-

PRACTICE NOTE

ESTs are recognized in the art as small pieces of DNA sequence (usually 200 to 500 nucleotides long) that are generated by sequencing either one or both ends of an expressed gene. The idea is to sequence bits of DNA that represent genes expressed in certain cells, tissues, or organs. These "tags" are used to "fish out" a gene from a portion of chromosomal DNA by matching base pairs. See, e.g., www.ncbi.nlm.nih.gov/About/primer/est.html, "Just the Facts: A Basic Introduction to the Science Underlying NCBI Resources, ESTs: GENE DISCOVERY MADE EASIER."

EXAMPLE 4: EXPRESSION SEQUENCE TAGS

making a library of cDNAs encoding full length proteins using random primers in combination with primers based on the nucleic acid sequences of the three disclosed ESTs.

Claims:

Claim 1. An isolated nucleic acid comprising SEQ ID NO: 1.

Claim 2. An isolated nucleic acid consisting of SEQ ID NO: 1.

Analysis:

Claim 2

Because claim 2 uses the "closed" transitional term "consisting of" it encompasses a single species of isolated nucleic acid, *i.e.*, BKC1. The specification discloses the complete structure of BKC1, *i.e.*, SEQ ID NO: 1. The specification also describes a method of isolating BKC1 from bladder and kidney cells. Because the specification discloses the complete structure of the claimed species, as well as a method of making it, those of ordinary skill in the EST art would recognize the inventor to have been in possession of the claimed nucleic acid at the time of filing.

Conclusion:

The specification satisfies the written description requirement of 35 U.S.C. 112, first paragraph, with respect to the full scope of claim 2.

Claim 1

Claim 1 encompasses a genus of isolated nucleic acids each having as part of its structure SEQ ID NO: 1. Because the claim uses the open transitional phrase "comprising," the claimed nucleic acids may also include additional DNA sequences at either end of the sequence shown in SEQ ID NO: 1. The genus, therefore, includes the full-length open reading frame that includes SEQ ID NO: 1, as well as fusion constructs and vectors comprising SEQ ID NO: 1. (The genus might include the full-length genomic gene. More specifically, if SEQ ID NO: 1 is derived from a single exon, the genomic sequence would comprise SEQ ID NO: 1; if SEQ ID NO: 1 is derived from more than one exon, the genomic sequence would not comprise SEQ ID NO: 1.)

There may be substantial variability among the species of DNAs encompassed by the scope of the claim because SEQ ID NO: 1 may be combined with other DNA sequences, but the scope of the genus is defined by the presence of the structure shown in SEQ ID NO: 1. Thus, all members of the genus will predictably include SEQ ID NO: 1.

The specification provides an actual reduction to practice and disclosure of one species within the genus; *i.e.*, the cDNA consisting of the sequence shown in SEQ ID NO: 1. That sequence also represents a partial structure of each DNA encompassed by the claimed genus: each member of the claimed genus must include SEQ ID NO: 1 as part of its structure because the presence of SEQ ID NO: 1 defines the scope of the claimed genus.